J'Faa

RAW SEQUENCE LISTING DATE: 07/09/2001
PATENT APPLICATION: **US/09/543,407** TIME: 12:43:42

Input Set : **A:\406.app.txt**
Output Set: **N:\CRF3\07092001\I543407.raw**

```
 4 <110> APPLICANT: White, Aaron P.
 5         Doran, James L.
 6         Collinson, S. Karen
 7         Kay, William W.
 9 <120> TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
10         PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
13 <130> FILE REFERENCE: 920043.406
15 <140> CURRENT APPLICATION NUMBER: US 09/543,407
16 <141> CURRENT FILING DATE: 2000-04-05
18 <160> NUMBER OF SEQ ID NOS: 59
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 456
24 <212> TYPE: DNA
25 <213> ORGANISM: Salmonella enteritidis
27 <400> SEQUENCE: 1
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29 ggcgtcgttc cacaatgggg cggcggcggt aatcataacg gcggcggcaa tagttccggc     120
30 ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa     180
31 agcgatgccc gtaaatctga aacgaccatt acccagagcg ttatggtaa cggcgccgat      240
32 gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaaataat     300
33 gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt     360
34 aataacgccg cgctggttaa tcagaccgca tctgattcca gcgtaatggt gcgtcaggtt     420
35 ggttttggca acaacgccac ggctaaccag tattaa                               456
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 456
39 <212> TYPE: DNA
40 <213> ORGANISM: Salmonella enteritidis
42 <400> SEQUENCE: 2
43 atgaaaaaca aattgttatt tatgatgttg acaatactgg gtgcgcctgg gattgcaacc      60
44 gcgacaaatt atgatctggc tcgttcagaa tataattttg cggtaaatga attaagcaag     120
45 tcttcattta atcaggcggc cattattggt caagtcggca cggataatag tgccagagta     180
46 cgccaggaag gatcaaaact attgtccgtt atttcacaag aaggaggaaa taatcgggcg     240
47 aaagtcgacc aggcagggaa ttataacttt gcgtatattg agcaaacggg caatgccaac     300
48 gatgccagta tatcgcaaag cgcttacggt aatagtgcag ctattatcca gaaaggttct     360
49 ggaaataagg ccaatattac ccagtacggt acgcagaaaa cagcagttgt agtgcagaaa     420
50 cagtcgcata tggctattcg cgtcacccaa cgctaa                               456
52 <210> SEQ ID NO: 3
53 <211> LENGTH: 456
54 <212> TYPE: DNA
55 <213> ORGANISM: E. Coli
57 <400> SEQUENCE: 3
58 atgaaacttt taaaagtaga agcaattgca gcaatcgtat tctccggtag cgctctggca      60
59 ggtgttgttc ctcagtacgg cggcggcggt aaccacggtg gtggcggtaa taatagcggc     120
60 ccaaattctg agctgaacat ttaccagtac ggtggcggta actctgcact tgctctgcaa     180
61 actgatgccc gtaactctga cttgactatt acccagcatg cggcggtaa tggtgcagat      240
62 gttggtcagg gctcagatga cagctcaatc gatctgaccc aacgtggctt cggtaacagc     300
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63 gctactcttg atcagtggaa cggcaaaaat tctgaaatga cggttaaaca gttcggtggt    360
64 ggcaacggtg ctgcagttga ccagactgca tctaactcct ccgtcaacgt gactcaggtt    420
65 ggctttggta acaacgcgac cgctcatcag tactaa                              456
67 <210> SEQ ID NO: 4
68 <211> LENGTH: 456
69 <212> TYPE: DNA
70 <213> ORGANISM: E. Coli
72 <400> SEQUENCE: 4
73 atgaaaaaca aattgttatt tatgatgtta acaatactgg gtgcgcctgg gattgcagcc     60
74 gcagcaggtt atgatttagc taattcagaa tataacttcg cggtaaatga attgagtaag    120
75 tcttcattta atcaggcagc cataattggt caagctggga ctaataatag tgctcagtta    180
76 cggcagggag gctcaaaact tttggcggtt gttgcgcaag aaggtagtag caaccgggca    240
77 aagattgacc agacaggaga ttataacctt gcatatattg atcaggcggg cagtgccaac    300
78 gatgccagta tttcgcaagg tgcttatggt aatactgcga tgattatcca gaaaggttct    360
79 ggtaataaag caaatattac acagtatggt actcaaaaaa cggcaattgt agtgcagaga    420
80 cagtcgcaaa tggctattcg cgtgacacaa cgttaa                              456
82 <210> SEQ ID NO: 5
83 <211> LENGTH: 151
84 <212> TYPE: PRT
85 <213> ORGANISM: Salmonella enteritidis
87 <400> SEQUENCE: 5
88 Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
89 1               5                   10                  15
90 Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
91              20                  25                  30
92 Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
93          35                  40                  45
94 Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
95      50                  55                  60
96 Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
97 65                  70                  75                  80
98 Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
99                  85                  90                  95
100 Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
101             100                 105                 110
102 Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
103         115                 120                 125
104 Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
105     130                 135                 140
106 Asn Ala Thr Ala Asn Gln Tyr
107 145                 150
109 <210> SEQ ID NO: 6
110 <211> LENGTH: 151
111 <212> TYPE: PRT
112 <213> ORGANISM: Salmonella enteritidis
114 <400> SEQUENCE: 6
115 Met Lys Asn Lys Leu Leu Phe Met Met Leu Thr Ile Leu Gly Ala Pro
116 1               5                   10                  15
117 Gly Ile Ala Thr Ala Thr Asn Tyr Asp Leu Ala Arg Ser Glu Tyr Asn
```

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```
118               20               25               30
119 Phe Ala Val Asn Glu Leu Ser Lys Ser Ser Phe Asn Gln Ala Ala Ile
120         35               40               45
121 Ile Gly Gln Val Gly Thr Asp Asn Ser Ala Arg Val Arg Gln Glu Gly
122     50               55               60
123 Ser Lys Leu Leu Ser Val Ile Ser Gln Glu Gly Gly Asn Asn Arg Ala
124 65               70               75               80
125 Lys Val Asp Gln Ala Gly Asn Tyr Asn Phe Ala Tyr Ile Glu Gln Thr
126             85               90               95
127 Gly Asn Ala Asn Asp Ala Ser Ile Ser Gln Ser Ala Tyr Gly Asn Ser
128             100              105              110
129 Ala Ala Ile Ile Gln Lys Gly Ser Gly Asn Lys Ala Asn Ile Thr Gln
130         115              120              125
131 Tyr Gly Thr Gln Lys Thr Ala Val Val Val Gln Lys Gln Ser His Met
132     130              135              140
133 Ala Ile Arg Val Thr Gln Arg
134 145              150

136 <210> SEQ ID NO: 7
137 <211> LENGTH: 151
138 <212> TYPE: PRT
139 <213> ORGANISM: Escherichia coli
141 <400> SEQUENCE: 7
142 Met Lys Leu Leu Lys Val Ala Ala Ile Ala Ala Ile Val Phe Ser Gly
143 1               5               10               15
144 Ser Ala Leu Ala Gly Val Val Pro Gln Tyr Gly Gly Gly Gly Asn His
145             20               25               30
146 Gly Gly Gly Gly Asn Asn Ser Gly Pro Asn Ser Glu Leu Asn Ile Tyr
147         35               40               45
148 Gln Tyr Gly Gly Gly Asn Ser Ala Leu Ala Leu Gln Thr Asp Ala Arg
149     50               55               60
150 Asn Ser Asp Leu Thr Ile Thr Gln His Gly Gly Gly Asn Gly Ala Asp
151 65               70               75               80
152 Val Gly Gln Gly Ser Asp Asp Ser Ser Ile Asp Leu Thr Gln Arg Gly
153             85               90               95
154 Phe Gly Asn Ser Ala Thr Leu Asp Gln Trp Asn Gly Lys Asn Ser Glu
155             100              105              110
156 Met Thr Val Lys Gln Phe Gly Gly Gly Asn Gly Ala Ala Val Asp Gln
157         115              120              125
158 Thr Ala Ser Asn Ser Ser Val Asn Val Thr Gln Val Gly Phe Gly Asn
159     130              135              140
160 Asn Ala Thr Ala His Gln Tyr
161 145              150

163 <210> SEQ ID NO: 8
164 <211> LENGTH: 151
165 <212> TYPE: PRT
166 <213> ORGANISM: Escherichia coli
168 <400> SEQUENCE: 8
169 Met Lys Asn Lys Leu Leu Phe Met Met Leu Thr Ile Leu Gly Ala Pro
170 1               5               10               15
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Input Set : A:\406.app.txt
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```
171 Gly Ile Ala Ala Ala Ala Gly Tyr Asp Leu Ala Asn Ser Glu Tyr Asn
172         20                  25                  30
173 Phe Ala Val Asn Glu Leu Ser Lys Ser Ser Phe Asn Gln Ala Ala Ile
174         35                  40                  45
175 Ile Gly Gln Ala Gly Thr Asn Asn Ser Ala Gln Leu Arg Gln Gly Gly
176     50                  55                  60
177 Ser Lys Leu Leu Ala Val Val Ala Gln Glu Gly Ser Ser Asn Arg Ala
178 65                  70                  75                  80
179 Lys Ile Asp Gln Thr Gly Asp Tyr Asn Leu Ala Tyr Ile Asp Gln Ala
180             85                  90                  95
181 Gly Ser Ala Asn Asp Ala Ser Ile Ser Gln Gly Ala Tyr Gly Asn Thr
182             100                 105                 110
183 Ala Met Ile Ile Gln Lys Gly Ser Gly Asn Lys Ala Asn Ile Thr Gln
184         115                 120                 125
185 Tyr Gly Thr Gln Lys Thr Ala Ile Val Val Gln Arg Gln Ser Gln Met
186     130                 135                 140
187 Ala Ile Arg Val Thr Gln Arg
188 145                 150
190 <210> SEQ ID NO: 9
191 <211> LENGTH: 48
192 <212> TYPE: DNA
193 <213> ORGANISM: Leishmania major
195 <400> SEQUENCE: 9
196 tatgatcagc tggttacccg tgttgttacc catgaaatgg cacatgca                48
198 <210> SEQ ID NO: 10
199 <211> LENGTH: 16
200 <212> TYPE: PRT
201 <213> ORGANISM: Leishmania major
203 <400> SEQUENCE: 10
204 Tyr Asp Gln Leu Val Thr Arg Val Val Thr His Glu Met Ala His Ala
205 1               5                   10                  15
207 <210> SEQ ID NO: 11
208 <211> LENGTH: 456
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
214         sequence containing the replacement fragment
215         encoding PT3 from GP63 of Leishmania major.
217 <400> SEQUENCE: 11
218 atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct    60
219 ggcgtcgttc cacaatgggg cggcggcggt aatcataacg gcggcggcaa tagttccggc   120
220 ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa   180
221 agcgatgccc gtaaatctga aacgaccatt acccagagcg gttatggtaa cggcgccgat   240
222 gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaaataat   300
223 gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt   360
224 aataacgccg cgctggttaa ttatgatcag ctggttaccc gtgttgttac ccatgaaatg   420
225 gcacatgcaa acaacgccac ggctaaccag tattaa                            456
227 <210> SEQ ID NO: 12
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RAW SEQUENCE LISTING
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228 <211> LENGTH: 151
229 <212> TYPE: PRT
230 <213> ORGANISM: Artificial Sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
234       sequence containing the replacement fragment
235       encoding PT3 from GP63 of Leishmania major.
237 <400> SEQUENCE: 12
238 Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
239 1               5                   10                  15
240 Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
241         20                  25                  30
242 Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
243         35                  40                  45
244 Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
245     50                  55                  60
246 Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
247 65                  70                  75                  80
248 Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
249                 85                  90                  95
250 Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
251             100                 105                 110
252 Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Tyr
253             115                 120                 125
254 Asp Gln Leu Val Thr Arg Val Val Thr His Glu Met Ala His Ala Asn
255     130                 135                 140
256 Asn Ala Thr Ala Asn Gln Tyr
257 145                 150
259 <210> SEQ ID NO: 13
260 <211> LENGTH: 456
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
266       sequence containing the replacement fragment
267       encoding PT3 from GP63 of Leishmania major..
269 <400> SEQUENCE: 13
270 atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct      60
271 ggcgtcgttc cacaatgggg cggcggcggt aatcataacg gcggcggcaa tagttccggc     120
272 ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa     180
273 agcgatgccc gtaaatctga aacgaccatt acccagagcg gttatggtaa cggcgccgat     240
274 gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaaataat     300
275 gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atatgatcag     360
276 ctggttaccc gtgttgttac ccatgaaatg gcacatgcaa cgtaatggt gcgtcaggtt       420
277 ggttttggca acaacgccac ggctaaccag tattaa                                456
279 <210> SEQ ID NO: 14
280 <211> LENGTH: 151
281 <212> TYPE: PRT
282 <213> ORGANISM: Artificial Sequence
```

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 07/09/2001
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```
L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59
L:1149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59
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